

SEQUENCE LISTING

O I P E 14P38
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PATENT & TRADEMARK OFFICE
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VERNET, THIERRY
MOUZ, NICOLAS

<1520> STREPTOCOCCUS PNEUMONIAE PBP2X MINI-PROTEIN AND USES
THEREOF

<130> 70457-19

<140> 10/520,655
<141> 2005-03-07

<150> PCT/IB03/003397
<151> 2003-07-11

<150> FR 02/08724
<151> 2002-07-11

<160> 18

<170> PatentIn Ver. 3.3

<210> 1
<211> 551
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
mini-PBP2x construct

<400> 1
Gly Ser Gly Ala Lys Arg Gly Thr Ile Tyr Asp Arg Asn Gly Val Pro
1 5 10 15

Ile Ala Glu Asp Ala Thr Ser Gly Gly Pro Asn Arg Ser Tyr Pro Asn
20 25 30

Gly Gln Phe Ala Ser Ser Phe Ile Gly Gly Met Glu Ser Ser Leu
35 40 45

Asn Ser Ile Leu Ala Gly Gly Asp Gly Lys Asp Val Tyr Thr
50 55 60

Thr Ile Ser Ser Pro Leu Gln Ser Phe Met Glu Thr Gln Met Asp Ala
65 70 75 80

Phe Gln Glu Lys Val Lys Gly Lys Tyr Met Thr Ala Thr Leu Val Ser
85 90 95

Ala Lys Thr Gly Glu Ile Leu Ala Thr Thr Gln Arg Pro Thr Phe Asp
100 105 110

Ala Asp Thr Lys Glu Gly Ile Thr Glu Asp Phe Val Trp Arg Asp Ile
115 120 125

Leu Tyr Gln Ser Asn Tyr Glu Pro Gly Ser Thr Met Lys Val Met Met
 130 135 140
 Leu Ala Ala Ala Ile Asp Asn Asn Thr Phe Pro Gly Gly Glu Val Phe
 145 150 155 160
 Asn Ser Ser Glu Leu Lys Ile Ala Asp Ala Thr Ile Arg Asp Trp Asp
 165 170 175
 Val Asn Glu Gly Leu Thr Gly Gly Arg Met Met Thr Phe Ser Gln Gly
 180 185 190
 Phe Ala His Ser Ser Asn Val Gly Met Thr Leu Leu Glu Gln Lys Met
 195 200 205
 Gly Asp Ala Thr Trp Leu Asp Tyr Leu Asn Arg Phe Lys Phe Gly Val
 210 215 220
 Pro Thr Arg Phe Gly Leu Thr Asp Glu Tyr Ala Gly Gln Leu Pro Ala
 225 230 235 240
 Asp Asn Ile Val Asn Ile Ala Gln Ser Ser Phe Gly Gln Gly Ile Ser
 245 250 255
 Val Thr Gln Thr Gln Met Ile Arg Ala Phe Thr Ala Ile Ala Asn Asp
 260 265 270
 Gly Val Met Leu Glu Pro Lys Phe Ile Ser Ala Ile Tyr Asp Pro Asn
 275 280 285
 Asp Gln Thr Ala Arg Lys Ser Gln Lys Glu Ile Val Gly Asn Pro Val
 290 295 300
 Ser Lys Asp Ala Ala Ser Leu Thr Arg Thr Asn Met Val Leu Val Gly
 305 310 315 320
 Thr Asp Pro Val Tyr Gly Thr Met Tyr Asn His Ser Thr Gly Lys Pro
 325 330 335
 Thr Val Thr Val Pro Gly Gln Asn Val Ala Leu Lys Ser Gly Thr Ala
 340 345 350
 Gln Ile Ala Asp Glu Lys Asn Gly Gly Tyr Leu Val Gly Leu Thr Asp
 355 360 365
 Tyr Ile Phe Ser Ala Val Ser Met Ser Pro Ala Glu Asn Pro Asp Phe
 370 375 380
 Ile Leu Tyr Val Thr Val Gln Gln Pro Glu His Tyr Ser Gly Ile Gln
 385 390 395 400
 Leu Gly Glu Phe Ala Asn Pro Ile Leu Glu Arg Ala Ser Ala Met Lys
 405 410 415
 Asp Ser Leu Asn Leu Gln Thr Thr Ala Lys Ala Leu Glu Gln Val Ser
 420 425 430

Gln Gln Ser Pro Tyr Pro Met Pro Ser Val Lys Asp Ile Ser Pro Gly
 435 440 445

 Asp Leu Ala Glu Glu Leu Arg Arg Asn Leu Val Gln Pro Ile Val Val
 450 455 460

 Gly Thr Gly Thr Lys Ile Lys Asn Ser Ser Ala Glu Glu Gly Lys Asn
 465 470 475 480

 Leu Ala Pro Asn Gln Gln Val Leu Ile Leu Ser Asp Lys Ala Glu Glu
 485 490 495

 Val Pro Asp Met Tyr Gly Trp Thr Lys Glu Thr Ala Glu Thr Leu Ala
 500 505 510

 Lys Trp Leu Asn Ile Glu Leu Glu Phe Gln Gly Ser Gly Ser Thr Val
 515 520 525

 Gln Lys Gln Asp Val Arg Ala Asn Thr Ala Ile Lys Asp Ile Lys Lys
 530 535 540

 Ile Thr Leu Thr Leu Gly Asp
 545 550

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<210> 2
<211> 46
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<220>
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      primer

<400> 2
gtcgacttag tctcctaaag ttaatttaat tttttaatg tttttg                  46

<210> 3
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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<400> 3
ggatccggga caggcactcg c                  21

<210> 4
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<220>
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<400> 4
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<210> 5
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 5
gttggtaa ctacgattgg gacctccaga ggttgcattc tcagcaatcg g      51

<210> 6
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
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<400> 6
gttcaaggaa ctctccattc caccggcat aaaactagaa gcaaattg          48

<210> 7
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
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<400> 7
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<210> 8
<211> 30
<212> DNA
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<220>
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<220>
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<210> 10
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (3)
<223> variable amino acid

<220>
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<222> (4)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (5)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (6)
<223> Asp or Ser

<220>
<221> MOD_RES
<222> (10)..(12)
<223> variable amino acid

<400> 10
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<210> 11
<211> 6
<212> PRT
<213> Artificial Sequence
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<220>
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      peptide

<220>
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<222> (1)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (2)..(3)
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<220>
<221> MOD_RES
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<223> variable amino acid

<400> 11
Xaa Xaa Xaa Pro Xaa Gly
    1           5

<210> 12
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MOD_RES
<222> (1)
<223> Gly or Tyr

<220>
<221> MOD_RES
<222> (2)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (4)..(6)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (8)..(9)
<223> variable amino acid

<400> 12
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    1           5           10
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<210> 13
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (1)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (2)..(3)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (4)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (5)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (7)..(9)
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<400> 13
Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Gln
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<210> 14
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (2)
<223> Gly or Ser

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<222> (4)..(5)
<223> hydrophobic amino acid
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<220>
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<222> (6)..(9)
<223> variable amino acid

<220>
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<223> variable amino acid

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<223> hydrophobic amino acid

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<222> (14)
<223> Asp or Asn

<400> 14
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    1           5           10

<210> 15
<211> 8
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<220>
<223> Description of Artificial Sequence: Synthetic
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<220>
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<223> Ala or Gly

<220>
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<222> (6)..(7)
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<400> 15
Xaa Glu Pro Xaa Ser Xaa Xaa Lys
    1           5
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<210> 16
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
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<222> (2)..(3)
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<220>
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<223> variable amino acid

<220>
<221> MOD_RES
<222> (7)
<223> hydrophobic amino acid

<400> 16
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1 5

<210> 17
<211> 7
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 17
Ala Lys Arg Gly Thr Ile Tyr
1 5

<210> 18
<211> 750
<212> PRT
<213> Streptococcus pneumoniae

<400> 18
Met Lys Trp Thr Lys Arg Val Ile Arg Tyr Ala Thr Lys Asn Arg Lys
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Ser Pro Ala Glu Asn Arg Arg Arg Val Gly Lys Ser Leu Ser Leu Leu
 20 25 30

Ser Val Phe Val Phe Ala Ile Phe Leu Val Asn Phe Ala Val Ile Ile
 35 40 45

Gly Thr Gly Thr Arg Phe Gly Thr Asp Leu Ala Lys Glu Ala Lys Lys
 50 55 60

Val His Gln Thr Thr Arg Thr Val Pro Ala Lys Arg Gly Thr Ile Tyr
 65 70 75 80

Asp Arg Asn Gly Val Pro Ile Ala Glu Asp Ala Thr Ser Tyr Asn Val
 85 90 95

Tyr Ala Val Ile Asp Glu Asn Tyr Lys Ser Ala Thr Gly Lys Ile Leu
 100 105 110

Tyr Val Glu Lys Thr Gln Phe Asn Lys Val Ala Glu Val Phe His Lys
 115 120 125

Tyr Leu Asp Met Glu Glu Ser Tyr Val Arg Glu Gln Leu Ser Gln Pro
 130 135 140

Asn Leu Lys Gln Val Ser Phe Gly Ala Lys Gly Asn Gly Ile Thr Tyr
 145 150 155 160

Ala Asn Met Met Ser Ile Lys Lys Glu Leu Glu Ala Ala Glu Val Lys
 165 170 175

Gly Ile Asp Phe Thr Thr Ser Pro Asn Arg Ser Tyr Pro Asn Gly Gln
 180 185 190

Phe Ala Ser Ser Phe Ile Gly Leu Ala Gln Leu His Glu Asn Glu Asp
 195 200 205

Gly Ser Lys Ser Leu Leu Gly Thr Ser Gly Met Glu Ser Ser Leu Asn
 210 215 220

Ser Ile Leu Ala Gly Thr Asp Gly Ile Ile Thr Tyr Glu Lys Asp Arg
 225 230 235 240

Leu Gly Asn Ile Val Pro Gly Thr Glu Gln Val Ser Gln Arg Thr Met
 245 250 255

Asp Gly Lys Asp Val Tyr Thr Thr Ile Ser Ser Pro Leu Gln Ser Phe
 260 265 270

Met Glu Thr Gln Met Asp Ala Phe Gln Glu Lys Val Lys Gly Lys Tyr
 275 280 285

Met Thr Ala Thr Leu Val Ser Ala Lys Thr Gly Glu Ile Leu Ala Thr
 290 295 300

Thr Gln Arg Pro Thr Phe Asp Ala Asp Thr Lys Glu Gly Ile Thr Glu
 305 310 315 320

Asp Phe Val Trp Arg Asp Ile Leu Tyr Gln Ser Asn Tyr Glu Pro Gly
 325 330 335
 Ser Thr Met Lys Val Met Met Leu Ala Ala Ala Ile Asp Asn Asn Thr
 340 345 350
 Phe Pro Gly Gly Glu Val Phe Asn Ser Ser Glu Leu Lys Ile Ala Asp
 355 360 365
 Ala Thr Ile Arg Asp Trp Asp Val Asn Glu Gly Leu Thr Gly Gly Arg
 370 375 380
 Met Met Thr Phe Ser Gln Gly Phe Ala His Ser Ser Asn Val Gly Met
 385 390 395 400
 Thr Leu Leu Glu Gln Lys Met Gly Asp Ala Thr Trp Leu Asp Tyr Leu
 405 410 415
 Asn Arg Phe Lys Phe Gly Val Pro Thr Arg Phe Gly Leu Thr Asp Glu
 420 425 430
 Tyr Ala Gly Gln Leu Pro Ala Asp Asn Ile Val Asn Ile Ala Gln Ser
 435 440 445
 Ser Phe Gly Gln Gly Ile Ser Val Thr Gln Thr Gln Met Ile Arg Ala
 450 455 460
 Phe Thr Ala Ile Ala Asn Asp Gly Val Met Leu Glu Pro Lys Phe Ile
 465 470 475 480
 Ser Ala Ile Tyr Asp Pro Asn Asp Gln Thr Ala Arg Lys Ser Gln Lys
 485 490 495
 Glu Ile Val Gly Asn Pro Val Ser Lys Asp Ala Ala Ser Leu Thr Arg
 500 505 510
 Thr Asn Met Val Leu Val Gly Thr Asp Pro Val Tyr Gly Thr Met Tyr
 515 520 525
 Asn His Ser Thr Gly Lys Pro Thr Val Thr Val Pro Gly Gln Asn Val
 530 535 540
 Ala Leu Lys Ser Gly Thr Ala Gln Ile Ala Asp Glu Lys Asn Gly Gly
 545 550 555 560
 Tyr Leu Val Gly Leu Thr Asp Tyr Ile Phe Ser Ala Val Ser Met Ser
 565 570 575
 Pro Ala Glu Asn Pro Asp Phe Ile Leu Tyr Val Thr Val Gln Gln Pro
 580 585 590
 Glu His Tyr Ser Gly Ile Gln Leu Gly Glu Phe Ala Asn Pro Ile Leu
 595 600 605
 Glu Arg Ala Ser Ala Met Lys Asp Ser Leu Asn Leu Gln Thr Thr Ala
 610 615 620

Lys Ala Leu Glu Gln Val Ser Gln Gln Ser Pro Tyr Pro Met Pro Ser
625 630 635 640

Val Lys Asp Ile Ser Pro Gly Asp Leu Ala Glu Glu Leu Arg Arg Asn
645 650 655

Leu Val Gln Pro Ile Val Val Gly Thr Gly Thr Lys Ile Lys Asn Ser
660 665 670

Ser Ala Glu Glu Gly Lys Asn Leu Ala Pro Asn Gln Gln Val Leu Ile
675 680 685

Leu Ser Asp Lys Ala Glu Glu Val Pro Asp Met Tyr Gly Trp Thr Lys
690 695 700

Glu Thr Ala Glu Thr Leu Ala Lys Trp Leu Asn Ile Glu Leu Glu Phe
705 710 715 720

Gln Gly Ser Gly Ser Thr Val Gln Lys Gln Asp Val Arg Ala Asn Thr
725 730 735

Ala Ile Lys Asp Ile Lys Lys Ile Thr Leu Thr Leu Gly Asp
740 745 750